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**Fig.1**

Alignment of the BASB029 polynucleotide sequences.  
Identity to SeqID No:1 is indicated by a dot, and a dash ("-") indicates a missing nucleotide.

```

                *      20      *      40      *
Seqid1:ATGAACAAAATATAACCGCATCATTTGGAATAGTGCCCTCAATGCCTGGGT:50
Seqid3:.....:50

                60      *      80      *      100
Seqid1:CGCCGTATCCGAGCTCACACGCAACCACACCAAACGCGCCTCCGCAACCG:100
Seqid3:.....:100

                *      120      *      140      *
Seqid1:TGGCGACCGCCGTATTGGCGACACTGTTGTTTGCAACGGTTCAGGCGAGT:150
Seqid3:..AA.....A....:150

                160      *      180      *      200
Seqid1:ACTACCGAT-----GACGACGATTTATATTTAGAACCCGTACAACG:191
Seqid3:G...A.A..GAAGAGCAA..A..A.....C.....:200

                *      220      *      240      *
Seqid1:CACTGCTGTCTGTGTTGAGCTTCCGTTCCGATAAAGAAGGCACGGGAGAAA:241
Seqid3:....T..C.....TAG..AA.....:250

                260      *      280      *      300
Seqid1:AAG---AAGTTACAGAAGATTCAAATTGGGGAGTATATTTGACAAGAAA:288
Seqid3:...AAA....AGA....A....G....C.....A..G.....:300

                *      320      *      340      *
Seqid1:GGAGTACTAACAGCCGGAACAAATCACCTCAAAGCCGGCGACAACCTGAA:338
Seqid3:.....A..GA.....:350
```

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360

\*

380

\*

400

Seqid1:AATCAAACAAAACACCAATGAAAACACCAATGCCAGTAGCTTCACCTACT:388

Seqid3:.....G..CA.A.....:382

\*

420

\*

440

\*

Seqid1:CGCTGAAAAAAGACCTCACAGATCTGACCAGTGTTGGAAGTGAATAA:438

Seqid3:.....:432

460

\*

480

\*

500

Seqid1:TCGTTTAGCGCAAACAGCAATAAAGTCAACATCACAAGCGACACCAAAGG:488

Seqid3:.....G.....:482

\*

520

\*

540

\*

Seqid1:CTTGAATTTTCGCGAAAAAACGGCTGAGACCAACGGCGACACCACGGTTC:538

Seqid3:.....T.....G.....G...G.....:532

560

\*

580

\*

600

Seqid1:ATCTGAACGGTATCGGTTGACTTTGACCGATACGCTGCTGAATACCGGA:588

Seqid3:..C.....T.....:582

\*

620

\*

640

\*

Seqid1:GCGACCACAAACGTAACCAACGACAACGTTACCGATGACGAGAAAAAACG:638

Seqid3:.....:632

660

\*

680

\*

Seqid11:TGCGGCAAGCGTTAAAGACGTATTAAACGCAGGCTGGAACATTAAAGGCG:688

Seqid3:.....:682

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\* 720 \* 740 \*  
Seqid1: TTAAACCCGGTACAACAGCTTCCGATAACGTTGATTTGTCCGCACTTAC:738  
Seqid3: .....:732

760 \* 780 \* 800  
Seqid1: GACACAGTCGAGTTCTTGAGCGCAGATACGAAAACAACGACTGTTAATGT:788  
Seqid3: .....:782

\* 820 \* 840 \*  
Seqid1: GGAAAGCAAAGACAACGGCAAGAGAACCGAAGTTAAAATCGGTGCGAAGA:838  
Seqid3: .....A.....:832

860 \* 880 \* 900  
Seqid1: CTTCTGTTATCAAAGAAAAAGACGGTAAGTTGGTTACTGGTAAAGACAAA:888  
Seqid3: .....T.....:882

\* 920 \* 940 \*  
Seqid1: GGCGAGAATGATTCTTCTACAGACAAAGGCGAAGGCTTAGTGACTGCAAA:938  
Seqid3: .....G.....G.....:932

960 \* 980 \* 1000  
Seqid1: AGAAGTGATTGATGCAGTAAACAAGGCTGGTTGGAGAATGAAAACAACAA:988  
Seqid: .....:982

\* 1020 \* 1040 \*  
Seqid1: CCGCTAATGGTCAAACAGGTCAAGCTGACAAGTTTGAAACCGTTACATCA:1038  
Seqid3: .....:1032

1060 \* 1080 \* 1100  
Seqid1: GGCACAAATGTAACCTTTGCTAGTGGTAAAGGTACAACCTGCGACTGTAAG:1088  
Seqid3: .....:1082

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\* 1120 \* 1140 \*

Seqid1:TAAAGATGATCAAGGCAACATCACTGTTATGTATGATGTAAATGTCGGCG:1138  
Seqid3:.....:1132

1160 \* 1180 \* 1200

Seqid1:ATGCCCTAAACGTCAATCAGCTGCAAAACAGCCGTTGGAATTTGGATTCC:1188  
Seqid3:.....:1182

\* 1220 \* 1240 \*

Seqid1:AAAGCGGTTGCAGGTTCTTCGGGCAAAGTCATCAGCGGCAATGTTTCGCC:1238  
Seqid3:.....:1232

1260 \* 1280 \* 1300

Seqid1:GAGCAAGGGAAAGATGGATGAAACCGTCAACATTAATGCCGGCAACAACA:1288  
Seqid3:.....:1282

\* 1320 \* 1340 \*

Seqid1:TCGAGATTACCCGCAACGGCAAAAATATCGACATCGCCACTTCGATGACC:1338  
Seqid3:.....T.....:1332

1360 \* 1380 \* 1400

Seqid1:CCGCAATTTTCCAGCGTTTCGCTCGGCGCGGGGGCGGATGCGCCCACTTT:1388  
Seqid3:.....G.....:1382

\* 1420 \* 1440 \*

Seqid1:AAGCGTGGATGACGAGGGCGCGTTGAATGTCGGCAGCAAGGATGCCAACA:1438  
Seqid3:G.....G..A..A.....A.G.A.....:1429

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1460

\*

1480

\*

1500

Seqid1:AACCCGTCCGCATTACCAATGTCGCCCCGGGCGTTAAAGAGGGGGATGTT:1488

Seqid3:.....:1479

\*

1520

\*

1540

\*

Seqid1:ACAAACGTGCGACAACCTTAAAGGCGTGGCGCAAACTTGAACAACCACAT:1538

Seqid3:.....G....:1529

1560

\*

1580

\*

1600

Seqid1:CGACAATGTGGACGGCAACGCGCGTGGGGCATCGCCCAAGCGATTGCAA:1588

Seqid3:.....:1579

\*

1620

\*

1640

\*

Seqid1:CCGCAGGTCTGGTTCAGGCGTATCTGCCCCGCAAGAGTATGATGGCGATC:1638

Seqid3:.....T.....:1629

1660

\*

1680

\*

1700

Seqid1:GGCGGCGGCACTTATCGCGGCGAAGCCGGTTATGCCATCGGCTACTCAAG:1688

Seqid3:.....C.....C...:1679

\*

1720

\*

1740

\*

Seqid1:CATTTCGACGGCGGAAATTGGATTATCAAAGGCACGGCTTCCGGCAATT:1738

Seqid3:T.....:1729

1760

\*

1780

\*

Seqid1:CGCGCGGCCATTTGGTGCTTCCGCATCTGTCGGTTATCAGTGGTAA:1785

Seqid3:.....:1776

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**Fig.2**

Alignment of the BASB029 polypeptide sequences.

Identity to SeqID No:2 is indicated by a dot, and a dash ("-") indicates a missing amino acid.

```
          *          20          *          40          *
Seqid2: MNKIYRIIWNSALNAWVAVSELTRNHTKRASATVATAVLATLLFATVQAS:50
Seqid4: .....K.....:50
```

```
          60          *          80          *          100
Seqid2: T--TDDDDLYLEPVQRTAVVLSFRSDKEGTGEKE-VTEDSNWGVYFDKK:96
Seqid4: ANNEEQEE....D.....VA..IVN.....K.E....A....E.:100
```

```
          *          120          *          140          *
Seqid2: GVLTAGTITLKAGDNLKIKQNTNENTNASSFTYSLKKDLTDLTSVGTEKL:146
Seqid4: .....RE.....-.....G N.....:144
```

```
          160          *          180          *          200
Seqid2: SFSANSNKVNITSDTKGLNFAKKTAE TNGD TTVHLNGIGSTLTD TLLNTG:196
Seqid4: .....G.....E..G.....:194
```

```
          *          220          *          240          *
Seqid2: ATTNVTNDNVTDDEKKRAASVKDVLNAGWNIKGVP GTTASDNVDFVRTY:246
Seqid4: .....:244
```

```
          260          *          280          *          300
Seqid2: DTVEFLSADTKTTTVNVESKDNGKRTEVKIGAKTSVIKEKDGLVTGKDK:296
Seqid4: .....:294
```

```
          *          320          *          340          *
Seqid2: GENDSSTDKGEGLVTAKEVIDAVNKAGWRMKT TTANGQTGQADKFETVTS:346
Seqid4: ...G...E.....:344
```

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360 \* 380 \* 400  
Seqid2:GTNVTFASGKGTTATVSKDDQGNITVMYDVNVGDALNVNQLQNSGWNLDS:396  
Seqid4:.....:394

\* 420 \* 440 \*  
Seqid2:KAVAGSSGKVISGNVSPSKGKMDETVNINAGNNIEITRNGKNIDIATSM:446  
Seqid4:.....:444

460 \* 480 \* 500  
Seqid2:PQFSSVSLGAGADAPTLSVDDEGALNVGSKDANKPVRITNVAPGVKEGDV:496  
Seqid4:.....GD-.....KD.....:493

\* 520 \* 540 \*  
Seqid2:TNVAQLKGVAQNLNNHIDNVDGNARAGIAQAIATAGLVQAYLPGKSMMAI:546  
Seqid4:.....R.....:543

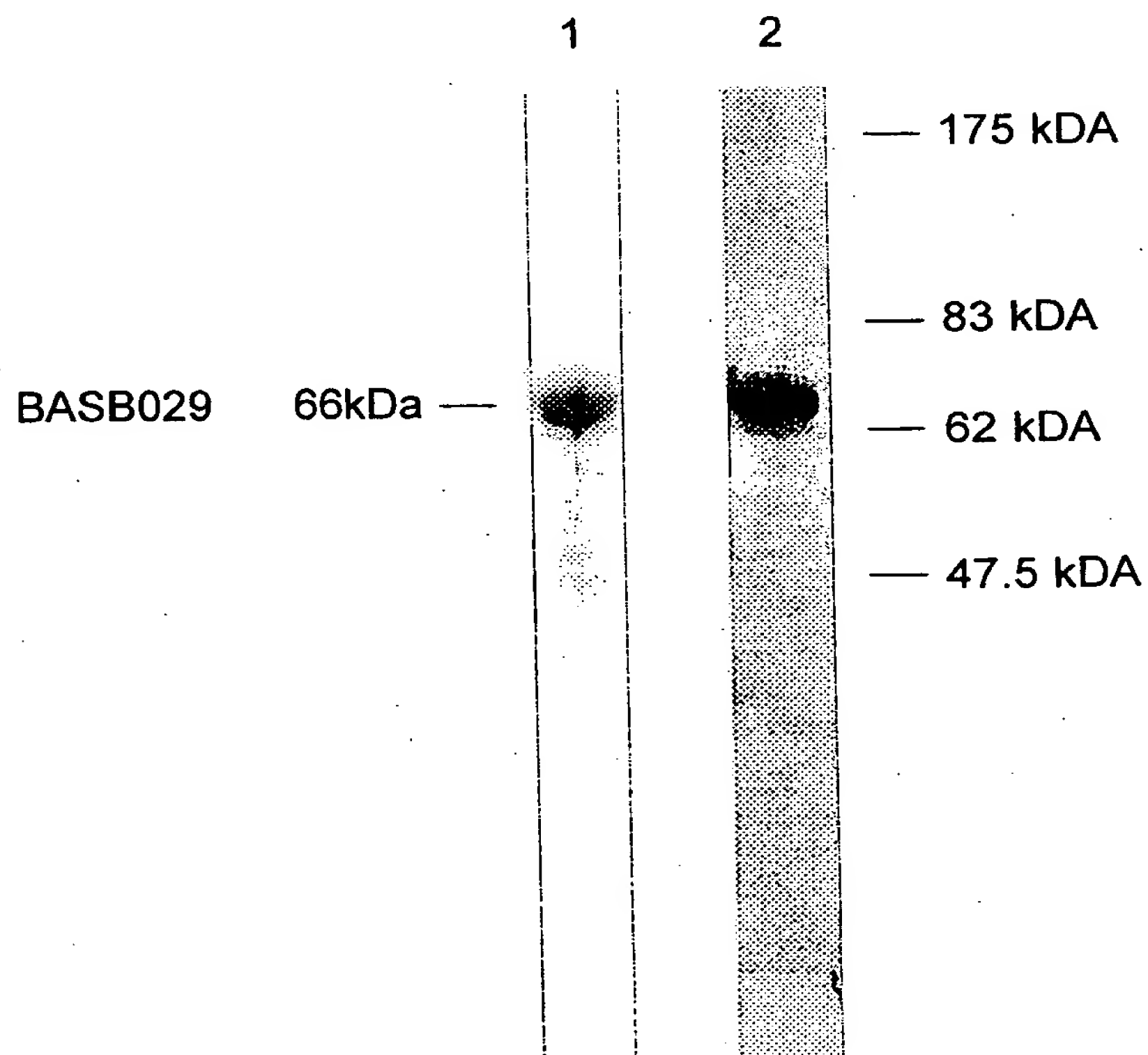
560 \* 580 \*  
Seqid2:GGGTYRGEAGYAIGYSSISDGGNWIIGKTASGNSRGHFGASASVGYQW:594  
Seqid4:.....:591



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**Fig.3** Expression and purification of recombinant BASB029 in E. coli.

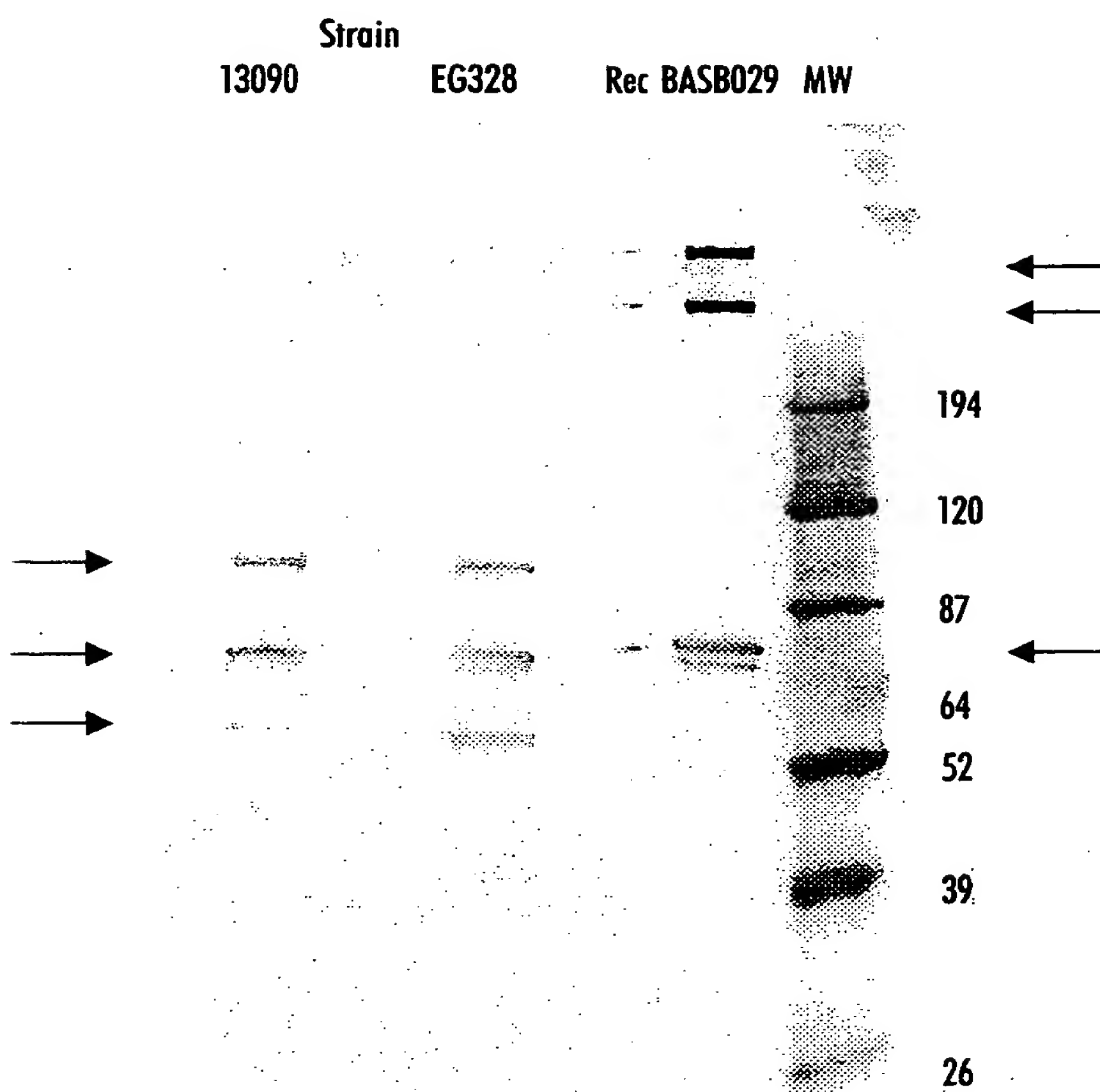
A substantially purified BASB029 protein fraction (more than 80%) was separated on a 4-20% gradient polyacrylamide gel (NOVEX) under PAGE-SDS conditions in parallel to a protein molecular weight marker. Gels were either stained with Coomassie Blue R250 (lane 1) or analyzed by western blot using an anti-(His5) monoclonal antibody (lane 2).



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# Fig.4

Recognition of the BASB029 protein on several NmB strains with BASB029 immunized mice sera



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**Fig.5**

Recognition of the BASB029 protein on several NmB strains with BASB029 immunized mice sera

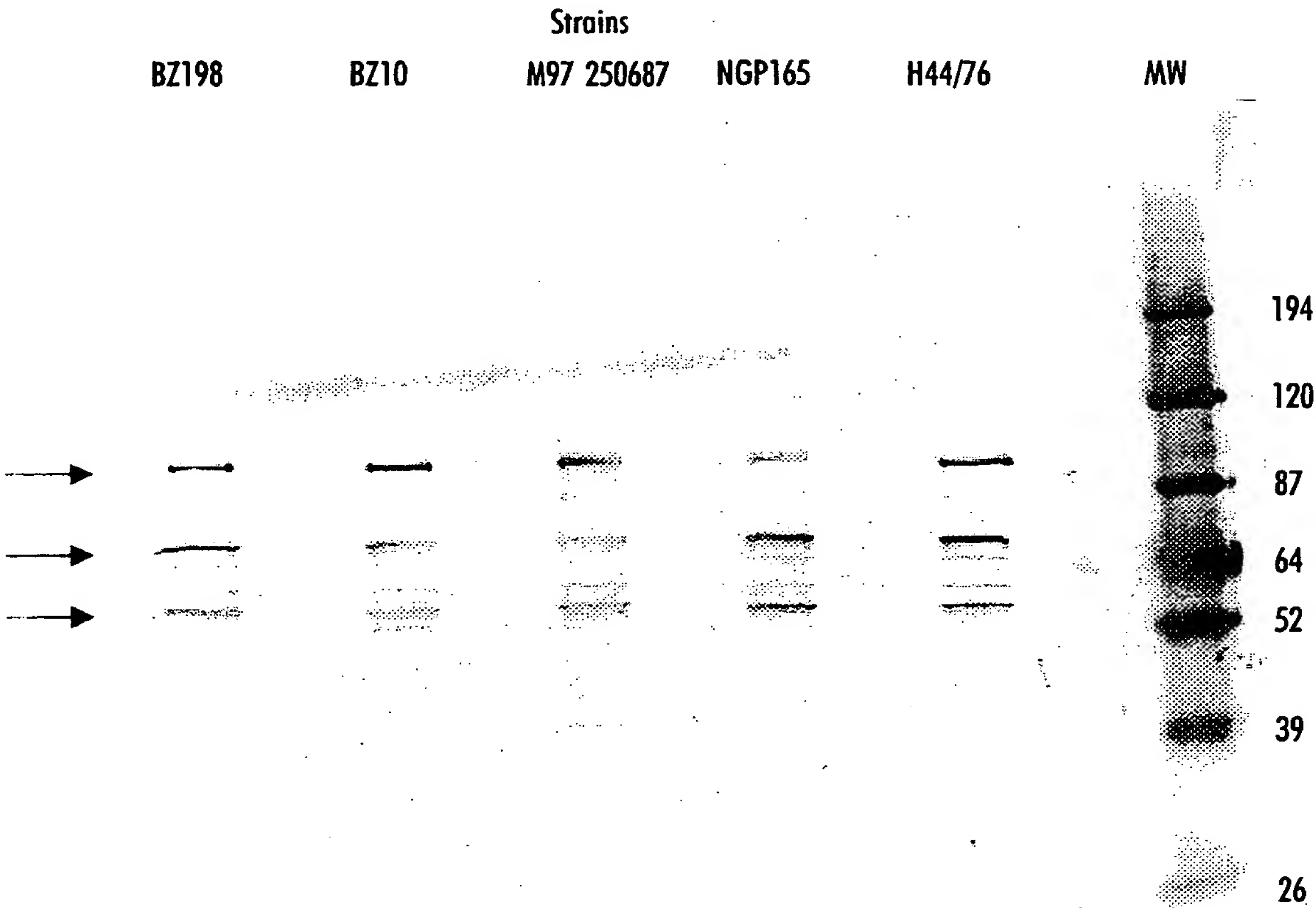
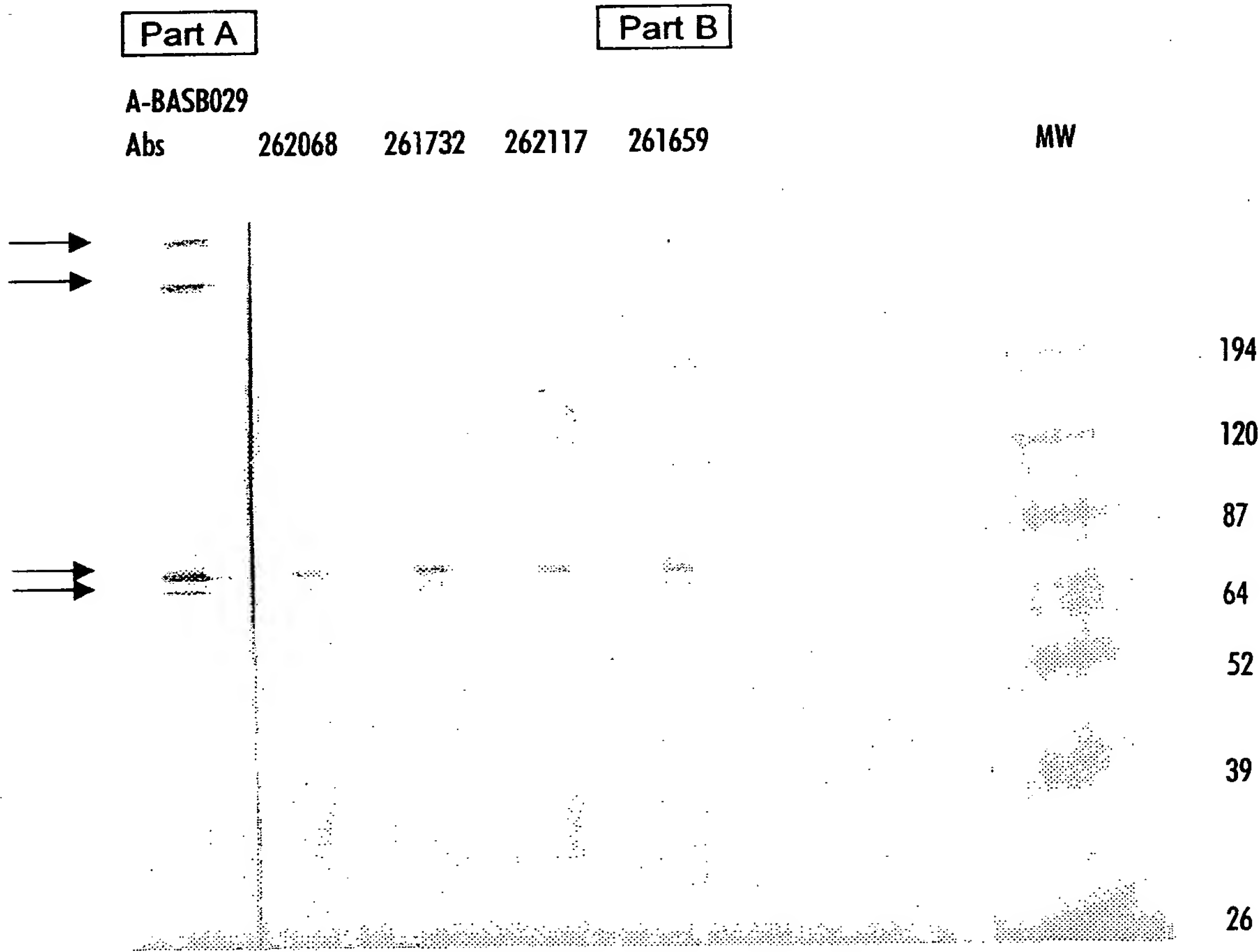


Fig.6

Anti-BASB029 antibodies in convalescent sera (part B) and in immunized mice (part A).



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**Fig.7**

Anti-BASB029 antibodies in convalescent sera (part B) and in immunized mice (part A).

